

Fig. 1

Human glycoprotein hormone β 10 polypeptide:

MKLAFLFLGPNMALLLLAGYGCVLGASSCNLRFTFVGCAVREFTFLLAKKPGCRGLRITTDACWRCETWEKPILEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVVAIRCDGACSTATTEC

Nucleic acid encoding human glycoprotein hormone β 10 polypeptide:

ATGAAGCTGGCATTCTCTTCTTGGCCCCCATGGCCCTCCTCCTTCTGGC
TGGCTATGGCTGTGTCCTCGGTGCTCCAGTGGAAACCTGCGCACCTTTG
TGGCTGTGCCGTGAGGAGTTTACTTCTTGGCCAAAGCCAGGCTGC
AGGGCCCTTCGGATCACACGGATGCTGCTGGGGTGGCTGTGAGACCTG
GGAGAAACCCATTCTGGAAACCCCTATATTGAAGCCCATCATCGAGTCT
GTACCTACAACGAGACCAACAGGTGACTGTCAAGCTGCCCAACTGTGCC
CCGGAGTCGACCCCTTCTACACCTATCCCGTGGCCATCCGCTGTGACTG
CGGAGCCTGCTCCACTGCCACCCACGGAGTGTGAGACCATCTGAGGCCGCT
AGCTGCTCTCTGCAGACCCACCTGTGTGAGCAGCACATGC

THEOREM

TO: HUMAN β_{10} CHECK: 6611 FROM: 1 TO: 106

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	129
RATIO:	1.321	GAPS:	4
PERCENT SIMILARITY:	47.368	PERCENT IDENTITY:	36.842

HUMAN TSH- β X HUMAN β 10

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1 .....FCIPTEYTMHIERRECAAYCLTINTTICAGYCMTRDINGKL 40
      | :| .: | | | | | | | | : :
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWE..KPI 47
.
41 FLPKYALSQD.VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCN 89
      | | . |||| : ||.:| | | |::.||| |: | | ||.
48 LEPPYIEAHRVCTYNETHKQVTVKLPNCAPGVDPFYTPVAIRCDGACS 97
.
90 TDYSDCIHEAIKTNCTKPQKSylvgfsv 118
      | .:| | |
98 TATTEC..ETI..... 106

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Fig. 2B

GAP OF: HUMAN FSH- β CHECK: 8841 FROM: 1 TO: 111
TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP
COMPCHECK: 6430

GAP WEIGHT: 8 AVERAGE MATCH: 2.912
LENGTH WEIGHT: 2 AVERAGE MISMATCH: -2.003
QUALITY: 156 LENGTH: 122
RATIO: 1.472 GAPS: 3
PERCENT SIMILARITY: 44.211 **PERCENT IDENTITY: 35.789**

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

| = IDENTITY
: = 2
. = 1

HUMAN FSH- β X HUMAN β 10

1NSCELTNITIAIEKEECRFCISINTTWCAGYCYTRDL.VYK 40
| . | . | | : | | | | : :
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEKPILE 49

41 DPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTPVATQCHCGKCDS 90
| : ||: | ||: | | | | | | . | | |
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDGACSTA 99

91 STDC.TVRGLGPSYCSFGEMKE 111
. | : | :
100 TTECETI..... 106

TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	125
RATIO:	1.321	GAPS:	3
PERCENT SIMILARITY:	44.118	PERCENT IDENTITY:	32.353

HUMAN LH- β X HUMAN β 10

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1  .SREPLRPW..CHPINAILAVEKEGCPVCITVNTTICAGYCPTMMR.VLQ 46
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1  ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEKPILE 49

47  AVLPPLPQVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRS 96
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
50  PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACSTA 99

97  TSDCGGPKDHPLTCDHPQLSGLLFL 121
   |  |  |
100  TTECETI..... 106

```

Fig. 2D

GAP OF: HUMAN CG- β CHECK: 2358 FROM: 1 TO: 145

TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP
COMPCHECK: 6430

GAP WEIGHT: 8 AVERAGE MATCH: 2.912
LENGTH WEIGHT: 2 AVERAGE MISMATCH: -2.003

QUALITY: 131 LENGTH: 149
RATIO: 1.236 GAPS: 3
PERCENT SIMILARITY: 42.157 **PERCENT IDENTITY: 31.373**

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
| = IDENTITY
: = 2
. = 1

HUMAN CG- β X HUMAN β 10

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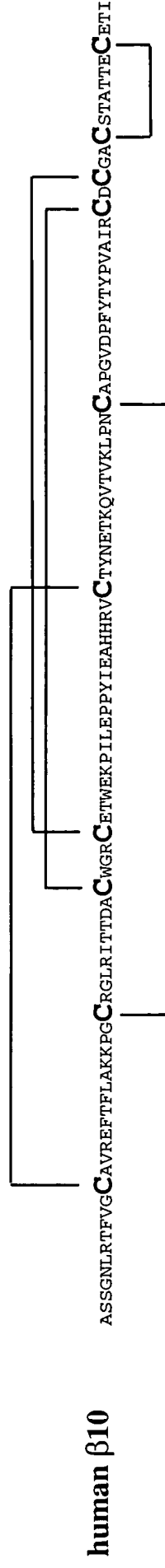
1 .SKEPLRP..RCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTR.VLQ 46
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEPILE 49

47 GVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 96
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACSTA 99

97 TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 145
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
100 TTECETI..... 106
  
```

09818954.032704

Fig. 3



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to: mouse β 10 check: 7740 from: 1 to: 106

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	577	Length:	106
Ratio:	5.443	Gaps:	0
Percent Similarity:	97.170	Percent Identity:	93.396

human $\beta 10$ x mouse $\beta 10$

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1  ASSGNLRTFVGCAVREFTFLAKKPGCRGLRITTDACWGRCEWTKPILEP  50
1  .|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  50
1  SSSGNLHTFVGCAVREFTFMAKKPGCRGLRITTDACWGRCEWTKPILEP  50

51  PYIEAHHRVCTYNETHQVTVKLPNCAPGVDPFYTYTPVAIRCDGACSTAT  100
51  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  100
51  PYIEAYHRVCTYNETHQVTVKLPNCAPGVDPFYTYTPMAVRCDGACSTAT  100

101  TECETI 106
101  |||||
101  TECETI 106

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